

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 00:24:09 : Search time 4358.45 Seconds
(without alignments)
11318.063 Million cell updates/sec

Title: US-09-856-979-6

Perfect score: 1695

Sequence: 1 ccgcagatcctctctgtgtga.....tccatcaagccgtcgcatg 1695

Scoring table: IDENTITY_MDC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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41: em_htgo_other:*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1695	100.0	1695	6	BD013095	BD013095 Method fo
2	1695	100.0	1695	23	BD010123	Bd010123 Method fo
3	1695	100.0	2275	6	BD013093	BD013093 Method fo
4	1695	100.0	2275	23	BD010121	Bd010121 Method fo
5	1695	100.0	5349	6	A71437	A71437 Sequence 7
6	1695	100.0	5349	6	AR207455	AR207455 Sequence
7	1695	100.0	6539	6	E31991	E31991 Mutated bar
8	1695	100.0	6548	6	A60109	A60109 Sequence 2
9	1695	100.0	6548	6	A76916	A76916 Sequence 2
10	1695	100.0	6548	6	AR098308	AR098308 Sequence
11	1695	100.0	6548	6	E31990	E31990 Mutated bar
12	1695	100.0	7492	6	BD013094	BD013094 Method fo
13	1695	100.0	7492	23	BD010122	Bd010122 Method fo
14	1693.4	99.9	2407	6	A23333	A23333 E1 gene, TA
15	1693.4	99.9	2407	6	AR007519	AR007519 Sequence
16	1693.4	99.9	2407	6	AR084085	AR084085 Sequence
17	1693.4	99.9	2407	6	I47736	I47736 Sequence 8
18	1693.4	99.9	170226	8	AP003450	AP003450 Oryza sat
19	1690.4	99.7	6667	6	AX118825	AX118825 Sequence
20	1687	99.5	1687	6	AX118836	AX118836 Sequence
21	365	21.5	365	6	BD013096	BD013096 Method fo
22	365	21.5	365	23	BD010124	Bd010124 Method fo
23	365	21.5	5228	6	BD013092	BD013092 Method fo
24	365	21.5	5228	23	BD010120	Bd010120 Method fo
25	234	13.8	141942	2	AC130725	AC130725 Oryza sat
26	100.8	5.9	34067	8	AP000414	AP000414 Arabidops
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30	81.8	4.8	159440	8	AP002900	AP002900 Oryza sat
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ALIGNMENTS

RESULT 1
BD013095
LOCUS BD013095 1695 bp DNA linear PAT 02-AUG-2002
DEFINITION Method for producing male-sterile plant.
ACCESSION BD013095
VERSION BD013095.1 GI:22093284
KEYWORDS WO 0124616-A/6.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 1695)
Hamada, K. and Nakakido, F.
Method for producing male-sterile plant

JOURNAL Patent: WO 0124616-A 6 12-APR-2001;
JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO
COMMENT OS Oryza sativa (rice)
PN WO 0124616-A/6
PD 12-APR-2001
PF 12-SEP-2000 WO 2000JP006222
PR 30-SEP-1999 JP 99P 279307
PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
PC A01H5/00,C12N15/11,C12N15/63,C12N15/82
CC E1 promoter
FH Key location/Qualifiers.
FEATURES source location/Qualifiers
1. 1695
/organism="Oryza sativa"
/db_xref="taxon:4530"
BASE COUNT 503 a 384 c 357 g 451 t
ORIGIN
Query Match 100.0%; Score 1695; DB 6; length 1695;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGCAGATCCTTCTGTGATGTTTATTAATAATTATATTTATCTGGAATACCTACC 60
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DB 1 CCGCAGATCCTTCTGTGATGTTTATTAATAATTATATTTATCTGGAATACCTACC 60
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DB 121 TCCAACCACTTAATATCATAAACAATCTGATGTTAGTCCAGAAGCTATATTGAGTAGTG 180
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DB 301 GTTGGCACTGGAAGTGTTCATGTTTACATCTCTTAATTAACGTAGCAAGAGTAGAT 360
OY 361 TATTATGTACAGAGAAATCTTCAGATCTTTCACATGCAATGCTGTAAGAAGACAG 420
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DB 361 TATTATGTACAGAGAAATCTTCAGATCTTTCACATGCAATGCTGTAAGAAGACAG 420
OY 421 ATACAGTGTAGCTTAGTTTGTATAGGAGGTCATGCCATTTCTCTGAAGGATGTTGAG 480
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DB 421 ATACAGTGTAGCTTAGTTTGTATAGGAGGTCATGCCATTTCTCTGAAGGATGTTGAG 480
OY 481 AGATGATGATTTCTGGGATCCTTGGAGGGGGCCCTGAATTCGGAACAAGTACGTTGAGTT 540
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DB 481 AGATGATGATTTCTGGGATCCTTGGAGGGGGCCCTGAATTCGGAACAAGTACGTTGAGTT 540
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DB 781 TTCCTGTCTTCCACAGCAGAAATATCCGCACTGCATAGCTCCCAACAATGAATCCCAA 840
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DB 841 ACCACATCGGCTCAGAGAGAAGTTATGATAAAAGGCACTAATCTGATTAATTTCTCTAGA 900
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DB 1201 AAACGAATACAGTTACCTTACCAGATGTTTGGCCACGACATGGGCCAAGCTCATGCTAGAC 1260
OY 1261 CAAGAAGGCAAGAGCAAAAGTTAGCTGTCAAAAAAGATATGCTAGAGGCTTTCAGAAAT 1320
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OY 1561 GCTTGCACCGTGACTCACTGCCACATTTGCCCGCGCGCTGCGCGGCGCTACAAAAGCCA 1620
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OY 1681 CAAGCGGTGCGGATG 1695
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DB 1681 CAAGCGGTGCGGATG 1695

RESULT 2
BD010123
ID BD010123 standard: DNA; PLN: 1695 BP.
XX BD010123;
AC BD010123;
XX
SV BD010123.1

XX 08-FEB-2002 (Rel. 70, created)
DT 08-FEB-2002 (Rel. 70, last updated, version 1)
XX
XX Method for producing male-sterile plant.
XX
KW JP 03075934-T/6.
XX
XX Oryza sativa
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae;
OC Oryzeae; Oryza.
XX
XX [1]
RN 1-1695
RA Hamada K., Nakakido F.;
RT "Method for producing male-sterile plant";
RL patent number JP03075934-T/6, 16-MAR-2001.
RL JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO.
XX
XX OS Oryza sativa (rice)
CC PN JP 03075934-T/6
CC PD 16-MAR-2001
CC PF 12-SEP-2000 JP 2000006222
CC PR 30-SEP-1999 JP 99P 279307
CC PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
CC PC A01H5/00,C12N15/11,C12N15/63,C12N15/82
CC CC
CC FH Key Location/Qualifiers
CC FT source 1. 1695
CC FT /organism="Oryza sativa (rice)"
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FH FT source 1. 1695
FH FT /db_xref="taxon:4530"
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SQ Sequence 1695 BP: 503 A; 384 C; 357 G; 451 T; 0 other:

Query Match 100.0%; Score 1695; DB 23; Length 1695;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAATCGCCGCAATACCAATAGAGA 120
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DB 1141 AGCTTATCTGCCAAGCAAGATAGCTGTGCGCTGTGGGATTTGAGCCGTTGAAGGGAAC 1200
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RESULT 3
BD013093/c

LOCUS BD013093 2275 bp DNA linear PAT 02-AUG-2002
DEFINITION Method for producing male-sterile plant.
ACCESSION BD013093
VERSION BD013093.1 GI:22093282
KEYWORDS WO 0124616-A/4.
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 2275)
AUTHORS Hamada, K. and Nakakido, F.
TITLE Method for producing male-sterile plant
JOURNAL Patent: WO 0124616-A 4 12-Apr-2001;
JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO

COMMENT OS Artificial Sequence
PN WO 0124616-A/4
PD 12-APR-2001
PF 12-SEP-2000 WO 2000JP006222
PR 30-SEP-1999 JP 99P 279307
PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
PC A01H5/00, C12N15/11, C12N15/63, C12N15/82
CC E1-barstar-3' nos
FH Key

FEATURES
source location/Qualifiers
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/organism="synthetic construct"
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BASE COUNT 604 a 496 c 496 g 679 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; Length 2275;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC BD010121;	
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DT 08-FEB-2002 (Rel. 70, Created)	
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DE Method for producing male-sterile plant.	
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KW JP 03075934-T/4.	
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OC artificial sequence.	
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RL JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO.	
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CC PC A01H5/00,C12N15/11,C12N15/63,C12N15/82	
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Best Local Similarity	100.0%; Pred. No. 0;
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QY	361	TATATTGTACCAAGAGAAATCTCTTCAGATCTTTCCAACTGCAATGCTGTAAGAACAG	420
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RESULT 5
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DEFINITION Sequence 7 from Patent WO9810081.
ACCESSION A71437
VERSION A71437.1 GI:4775050
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 5349)
AUTHORS Michiels,F. and Williams,M.
TITLE IMPROVED BARSTAR GENE
JOURNAL Patent: WO 9810081-A 7 12-MAR-1998;
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source 1. 5349
location/Qualifiers
BASE COUNT 1339 a 1233 c 1290 g 1487 t
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Best Local Similarity 100.0%; Pred. No. 0;
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DEFINITION Sequence 7 from patent us 6372960.
ACCESSION AR207455
VERSION AR207455.1 GI:21506374
KEYWORDS
SOURCE Unknown.
ORGANISM Unkown.
REFERENCE 1 (bases 1 to 5349)
AUTHORS Michiels, F. and Williams, M.
TITLE Barstar gene
JOURNAL Patent: US 6372960-A 7 16-APR-2002;
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source location/Qualifiers
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BASE COUNT 1339 a 1233 c 1290 g 1487 t
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QY 1681 CAAGCGCTCGCGATG 1695
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Db 3958 CAAGCGCTCGCGATG 3972

RESULT 7
E31991/c
LOCUS E31991 6539 bp DNA linear PAT 18-JUN-2001
DEFINITION Mutated barnase gene and transgenic plant thereof.
ACCESSION E31991
VERSION E31991.1 GI:13021588
KEYWORDS JP 2000041682-A/4.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 6539)
AUTHORS Kazuyuki, H. and Fumio, N.
TITLE Mutated barnase gene and transgenic plant thereof
JOURNAL Patent: JP 2000041682-A 4 15-FEB-2000;
JAPAN TOBACCO INC

COMMENT
OS Escherichia coli LE392
PN JP 2000041682-A/4
PD 15-FEB-2000
PF 04-AUG-1998 JP 1998220060
PR

PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
PC C12N15/09, A01H5/00, C12N5/10, C12N9/22//((C12N5/10, C12R1:91), PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)

FEATURES
FT source location/Qualifiers
FT source 1. 6539
FT source location/Qualifiers
FT source 1. 6539
FT source location/Qualifiers
FT source 1. 6539

BASE COUNT 1755 a 1578 c 1519 g 1687 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; length 6539;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AATATATAGTACCTGTGTCAAGCTGCAAGAACTTCCAAATGCGGACAAATACCAATAGAGA 120
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QY 481 AGATGATGATTTCTGGGATCTTGGAGGGCCCTGAATTCGGAAGACAGTTAGTTGAGTT 540
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Db 3707 TACCATCTCCACAGAGAAATTAAGCTAATACCTGTCCAGAGAGTGGTGGCATTTGACCAA 3648
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QY 1681 CAAGCCGTGCGCATG 1695
Db 2627 CAAGCCGTGCGCATG 2613

RESULT 8
A60109/c A60109 6548 bp DNA circular PAT 22-OCT-1999
DEFINITION Sequence 2 from Patent WO9706267.
ACCESSION A60109
VERSION A60109.1 GI:3715125
KEYWORDS
SOURCE Plasmid PTS172.
ORGANISM Plasmid PTS172
REFERENCE 1 (bases 1 to 6548)
AUTHORS De,B.M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: WO 9706267-A 2 20-FEB-1997;
FEATURES
source 1..6548
/organism="Plasmid PTS172"
/db_xref="taxon:106340"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; Length 6548;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCAGATCCTTCTGTGATGTTTATTAATAATTAATATTAATCTGGAATACCTACC 60
Db 4316 CCGCAGATCCTTCTGTGATGTTTATTAATAATAATTAATATTAATCTGGAATACCTACC 4257

QY 61 AATATATAGAGACTTGTCAAGCTGCGAGAACTTCCCAATCCGCCACATACCATAGAGA 120
Db 4256 AATATATAGAGACTTGTCAAGCTGCGAGAACTTCCCAATCCGCCACATACCATAGAGA 4197
QY 121 TCCAACCACTTAATATATCAATAACAATCTGATGTTAGTCCAAACTATATAGTAGTG 180
Db 4196 TCCAACCACTTAATATATCAATAACAATCTGATGTTAGTCCAAACTATATAGTAGTG 4137
QY 181 AACACAATATGACATTTAATCATTTATGAGGATTTATGGCTAACCTCTGCAATTCATATTC 240
Db 4136 AACACAATATGACATTTAATCATTTATGAGGATTTATGGCTAACCTCTGCAATTCATATTC 4077
QY 241 GATGCGCTTAATCTGTCGAATTTTAGCGCTCCAGAAAGAAATGCAAAATCCTTGACAAAT 300
Db 4076 GATGCGCTTAATCTGTCGAATTTTAGCGCTCCAGAAAGAAATGCAAAATCCTTGACAAAT 4017
QY 301 GTTGGCACTGGAACCTGTTCCATGTTTTCATCTCTTATTAAGCTAGCAAAAGAGTAGAT 360
Db 4016 GTTGGCACTGGAACCTGTTCCATGTTTTCATCTCTTATTAAGCTAGCAAAAGAGTAGAT 3957
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Db 3956 TATTTATGACAGAGAAATCTCTTCAGATTCCTTCCACATGCAATGTCTTAAGAAGACAG 3897
QY 421 ATACAGTATGATGTTTGTATGAGCGGTCAATGCCATTTCTCTGAAGGCACTGTTCAG 480
Db 3896 ATACAGTATGATGTTTGTATGAGCGGTCAATGCCATTTCTCTGAAGGCACTGTTCAG 3837
QY 481 AGATGATGATTTCTGAGATCTTGGAGGGCCCTGAATAATCGGAACAGTTACTGAGTT 540
Db 3836 AGATGATGATTTCTGAGATCTTGGAGGGCCCTGAATAATCGGAACAGTTACTGAGTT 3777
QY 541 TTAGTACCTAATGCTTGGCTATATACGTGAATGCAATTTCTGAAGTGAAGTTTC 600
Db 3776 TTAGTACCTAATGCTTGGCTATATACGTGAATGCAATTTCTGAAGTGAAGTTTC 3717
QY 601 TACCATCTCCAGAGAAATGAAGCTAATACCTGTCCAGAGAGTGTGCGCATTTGACCAA 660
Db 3716 TACCATCTCCAGAGAAATGAAGCTAATACCTGTCCAGAGAGTGTGCGCATTTGACCAA 3657
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QY 901 AACGGAATTAATATAGCAACCTTGACCTCCACCAAGAAAGCTTGTGATGCACTGTGCGC 960
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QY 1081 ATCTGTTAGAGAGCATGCTTTATAGCACTTAATAAATGAGTATTAATCTCTCAAGG 1140
Db 3236 ATCTGTTAGAGAGCATGCTTTATAGCACTTAATAAATGAGTATTAATCTCTCAAGG 3177
QY 1141 AGCCTATACCTGCCAAGAAAGATAGCTTGGCCTGTGGGATTTGAGCCGTTGAAGGGAAC 1200

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DB 3176 ACCCTATACTGCCAAGAAAGATAGCTTGGCCTGTGGGATTTGAGCCGTTGAAGGAAC 3117
OY 1201 AAACGAATACAGTTACCTTACAGATGTTTCCACAGACATGGCAAGCTCATTTGCTAGAC 1260
DB 3116 AAACGAATACAGTTACCTTACAGATGTTTCCACAGACATGGCAAGCTCATTTGCTAGAC 3057
OY 1261 CAAGAAGGCAAGCAAGCAAGTTTACCTGTCAAAAAAGATATGCTAGAGGCTTTCCAGANT 1320
DB 3056 CAAGAAGGCAAGCAAGCAAGTTTACCTGTCAAAAAAGATATGCTAGAGGCTTTCCAGANT 2997
OY 1321 ATGTTCTATCTGAGCCAGACCAATGGGGCAAAATTTACTATTTGCCATACATTAAAC 1380
DB 2996 ATGTTCTATCTGAGCCAGACCAATGGGGCAAAATTTACTATTTGCCATACATTAAAC 2937
OY 1381 CACGTAAGAAGTCTACACATCACTGTTGAAAGGCTCTGTTTCCAGCAAGCGTGAG 1440
DB 2936 CACGTAAGAAGTCTACACATCACTGTTGAAAGGCTCTGTTTCCAGCAAGCGTGAG 2877
OY 1441 AATGCACCTAATGAGCGGAGACAGACTTCTTACCGCTACTACTGCTACATCCTGTAGAC 1500
DB 2876 AATGCACCTAATGAGCGGAGACAGACTTCTTACCGCTACTACTGCTACATCCTGTAGAC 2817
OY 1501 GGTGAGCGGCTGAGGCTTTCGCGCATGAGCCGCTGCTGTTGTTGCTGACATTCGCGCAC 1560
DB 2816 GGTGAGCGGCTGAGGCTTTCGCGCATGAGCCGCTGCTGTTGTTGCTGACATTCGCGCAC 2757
OY 1561 GCTTGCACCGCTGACTCACTGCGCACATTTGCCCGCGCGCTGCGCGGCTTACAAAGCCA 1620
DB 2756 GCTTGCACCGCTGACTCACTGCGCACATTTGCCCGCGCGCTGCGCGGCTTACAAAGCCA 2697
OY 1621 CACAGCGACCGCGCGCGCACAGATAACCCATCTAGCATCCCGGTGTCCAGCAAGAGATCCAT 1680
DB 2696 CACAGCGACCGCGCGCGCACAGATAACCCATCTAGCATCCCGGTGTCCAGCAAGAGATCCAT 2637
OY 1681 CAAGCCGTCGCGCATG 1695
DB 2636 CAAGCCGTCGCGCATG 2622

RESULT 9
A76916/c 548 bp DNA circular PAT 22-OCT-1999
LOCUS A76916
DEFINITION Sequence 2 from Patent EP0757102.
ACCESSION A76916
VERSION A76916.1 GI:6088713
KEYWORDS
SOURCE plasmid PTS172.
ORGANISM plasmid PTS172.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De,B.M.
TITLE GENETIC TRANSFORMATION USING A PARP INHIBITOR
JOURNAL Patent: EP 0757102-A 2 05-FEB-1997;
FEATURES
PLANT GENETIC SYSTEMS NV (BE)
location/Qualifiers
source 1..6548
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
Query Match 100.0%; Score 1695; DB 6; Length 6548;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 4136 AACACGAATAGCAATTAACATTTAGAGATTTATGGCTTAACCTCTGCAATTCATATTCT 4077
OY 241 GATGCGTCTAATCTGCTCAATTTTAGCGCTCCAGAAAGAAATTCACATCTTGGACAAT 300
DB 4076 GATGCGTCTAATCTGCTCAATTTTAGCGCTCCAGAAAGAAATTCACATCTTGGACAAT 4017
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DB 3656 ATGAGATTCACAAAGCATGCGCAAGATGGCAATCTGGCAAGAGCGGAATTAATATTGTAT 3597
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DB 3296 TAGCTTCTGTTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3237
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OY 1141 AGCCTATACCTCCAAAGAAAGCATAGCTTGGCTGTGGGATGAGCCGTTGAAGGGAAC 1200
DB 3176 AGCCTATACCTCCAAAGAAAGCATAGCTTGGCTGTGGGATGAGCCGTTGAAGGGAAC 3117
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QY 1201 AAACGAATACAGTTACCTTACCAGATGTTTCCACGACATGGGCAACGTCATTTGCTAGAC 1260
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Db 3116 AAACGAATACAGTTACCTTACCAGATGTTTCCACGACATGGGCAACGTCATTTGCTAGAC 3057
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Db 2696 CACACGACGGCGGCCACGATAACCCATCTAGCATCCCGGTGTCCAGCAAGAGATCCAT 2637
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Db 2636 CAAGCCGTCGGCATG 2622

RESULT 10
AR098308/c 6548 bp DNA linear PAT 14-FEB-2001
LOCUS AR098308
DEFINITION Sequence 2 from patent US 6074876.
ACCESSION AR098308
VERSION AR098308.1 GI:12807565
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De Block,M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: US 6074876-A 2 13-JUN-2000;
FEATURES
source 1.6548
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; Length 6548;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCAGATCCCTCTGTGTGATGTTGTTTATTAATAATTATATATGGAATACCTACC 60
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Db 3716 TACCATCTCCACAGGAATTAAGCTTAATACCTGTCCAAAGAGTGTGCGGATTTGACCA 3657
QY 661 ATGAAGATCACAAAGCATGGCAAGAAATGGCAATCTGGCAAAAGAGCGGAATTATATTGTAT 720
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Db 3656 ATGAAGATCACAAAGCATGGCAAGAAATGGCAATCTGGCAAAAGAGCGGAATTATATTGTAT 3597
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Db 3596 TCTACTACATCGAACAAGAACCATATCAATGTTGCCCCAGAGAGACCCCGCAGATTAAG 3537
QY 781 TTCTGTTCTTCCACAGCAGAAATATCCGCAACTGCATAGTCCCAACAATGAATGCCAAA 840
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Db 3536 TTCTGTTCTTCCACAGCAGAAATATCCGCAACTGCATAGTCCCAACAATGAATGCCAAA 3477
QY 841 ACCACATCGGCTCAGAGAGAAGTTATGATAAAAGGCACATAATTTCTGAATATTTCTCTAGA 900
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Db 3476 ACCACATCGGCTCAGAGAGAAGTTATGATAAAAGGCACATAATTTCTGAATATTTCTCTAGA 3417
QY 901 AAGCGAATTAATATAGCACACCTTGAACCTCCACCAGAAAGCTTTGTGATCGACTTGTCG 960
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Db 3416 AAGCGAATTAATATAGCACACCTTGAACCTCCACCAGAAAGCTTTGTGATCGACTTGTCG 3357
QY 961 CATGAATGCAATTTGACATTTGTCACCTGTGAGAAATCTCTGGAAAAATGAGAGAGCA 1020
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QY 1021 TAGCTTGTGTGTATGTGTGGGATTAATTAAGCTGCTAAACTTTGTTCTGTATCG 1080
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Db 3296 TAGCTTGTGTGTATGTGTGGGATTAATTAAGCTGCTAAACTTTGTTCTGTATCG 3237
QY 1081 ATCTGTTAGACAGCATCGCTTTTATTAAGCACTTAATAAATGTAGTATAATCTCTCAAG 1140
|||||
Db 3236 ATCTGTTAGACAGCATCGCTTTTATTAAGCACTTAATAAATGTAGTATAATCTCTCAAG 3177
QY 1141 AGCCTATAGTCCCAAGAAAGGATAGCTTGCCCTGTGGGATTTGAGCCGTTGAAGGGAGAC 1200
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Db 3176 AGCCTATAGTCCCAAGAAAGGATAGCTTGCCCTGTGGGATTTGAGCCGTTGAAGGGAGAC 3117
QY 1201 AAACGAATACAGTTACCTTACAGATGTTTCCACGACATGGGCAACGTCATTTGCTAGAC 1260
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Db 3116 AAACGAATACAGTTACCTTACAGATGTTTCCACGACATGGGCAACGTCATTTGCTAGAC 3057
QY 1261 CAAGAAGGCAAGAAGCAAGTTTACGTTCAAAAAAGATATGCTAGAGGCTTTCCAGAAT 1320

Db 3056 CAGAGGCAAGCAAGAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTCCAGAAAT 2597
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QY 1621 CACAGCAGCGCGGCAAGATACCCATCTCTAGCATCCCGGTGTCCAGCAAGAGATCCAT 1680
Db 2696 CACAGCAGCGCGGCAAGATACCCATCTCTAGCATCCCGGTGTCCAGCAAGAGATCCAT 2637
QY 1681 CAGCCGTCGCGATG 1695
Db 2636 CAGCCGTCGCGATG 2622

RESULT 11
E31990/c
LOCUS E31990 6548 bp DNA linear PAT 18-JUN-2001
DEFINITION Mutated barnase gene and transgenic plant thereof.
ACCESSION E31990
VERSION E31990.1 GI:13021587
KEYWORDS JP 2000041682-A/3.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 6548)
AUTHORS Kazuyuki, H. and Fumio, N.
TITLE Mutated barnase gene and transgenic plant thereof
JOURNAL Patent: JP 2000041682-A 3 15-FEB-2000;
JAPAN TOBACCO INC
OS Escherichia coli LE392
PN JP 2000041682-A/3
PD 15-FEB-2000
PF 04-AUG-1998 JP 1998220060
PR
PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
PC C12N15/09, A01H5/00, C12N5/10, C12N9/22, C12N5/10, C12R1:91), PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)
CC
FH Key 1. 6548 Location/Qualifiers
FT source 1. 6548
FT location/Qualifiers
FT /organism="Escherichia coli LE392".

FEATURES
Source 1. 6548
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; Length 6548;
Best local similarity 100.0%; Pred. NO. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCAGATCCTTCTGTGATGTTTATTAATTTAATATTTATCTGAATACCTACC 60
Db 1 CCGCAGATCCTTCTGTGATGTTTATTAATTTAATATTTATCTGAATACCTACC 60

Db 4316 CCGCAGATCCTTCTGTGATGTTTATTAATTTAATTTAATTTATCTGAATACCTACC 4257
QY 61 AATATATAGTAGACTGTGCAAGCTGCAAGAACTTCCATGCGCGCAATPACCAATAGAGA 120
Db 4256 AATATATAGTAGACTGTGCAAGCTGCAAGAACTTCCATGCGCGCAATPACCAATAGAGA 4197
QY 121 TCCAACGACCTTAATATCATTAACAATCTGATGTTAGTCCAGAACTATATTGAGTAGTG 180
Db 4196 TCCAACGACCTTAATATCATTAACAATCTGATGTTAGTCCAGAACTATATTGAGTAGTG 4137
QY 181 AACACAATAGCACATTAACATTTATGAGATTTATGGCTAACCTGCAATTTCAATATTCT 240
Db 4136 AACACAATAGCACATTTAATATTTATGAGATTTATGGCTAACCTGCAATTTCAATATTCT 4077
QY 241 GATCGCTAATCTGCTCAATTTTACGCTCCAGAAAGAAATTGCAATCTTGACCAAT 300
Db 4076 GATCGCTAATCTGCTCAATTTTACGCTCCAGAAAGAAATTGCAATCTTGACCAAT 4017
QY 301 GTTGGCACTGAGACTGTTGCATGTTTATCATCTCTTATTAACGTAAGCAAGAGTAGAT 360
Db 4016 GTTGGCACTGAGACTGTTGCATGTTTATCATCTCTTATTAACGTAAGCAAGAGTAGAT 3957
QY 361 TATTATGTACAGAGAGAAATCTTTCAGATCTTTCACATGCAATGTCGTAAGAAGACAG 420
Db 3956 TATTATGTACAGAGAGAAATCTTTCAGATCTTTCACATGCAATGTCGTAAGAAGACAG 3897
QY 421 ATACAGTGTAGCTTAGTTTGTAAATGAGCGTCAATGCCATTTCTGAAAGCATGTTACG 480
Db 3896 ATACAGTGTAGCTTAGTTTGTAAATGAGCGTCAATGCCATTTCTGAAAGCATGTTACG 3837
QY 481 AGATGATGATTTCTGGGATCCTTGGAGGGGCCCTGAATTCGGAACAGTTAGTTGAGTT 540
Db 3836 AGATGATGATTTCTGGGATCCTTGGAGGGGCCCTGAATTCGGAACAGTTAGTTGAGTT 3777
QY 541 TTAGTACCTAATGTCTTGGCTTATCTAGTGAATGGCATTTCTGTAAAGCTGAGTTTC 600
Db 3776 TTAGTACCTAATGTCTTGGCTTATCTAGTGAATGGCATTTCTGTAAAGCTGAGTTTC 3717
QY 601 TACCATCTCCACAGGAATTAAGCTAATACCTGTCCAAAGAGTGTGGCATTTGACCAA 660
Db 3716 TACCATCTCCACAGGAATTAAGCTAATACCTGTCCAAAGAGTGTGGCATTTGACCAA 3657
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QY 781 TTCCTGTTCTCCACAGCAGAAATATCCGCAACTGCATAGCTCCCAACAATGAATCCAAA 840
Db 3536 TTCCTGTTCTCCACAGCAGAAATATCCGCAACTGCATAGCTCCCAACAATGAATCCAAA 3477
QY 841 ACCACATCGGCTCAGAGAGAAGTTATGATAAAGGCACATAATCTGAATATTTCTAGAGA 900
Db 3476 ACCACATCGGCTCAGAGAGAAGTTATGATAAAGGCACATAATCTGAATATTTCTAGAGA 3417
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Db 3416 AAGCGAATTAATATAGCACACCTTGACCTCCACCAAGAACTTGTGATCGACCTGCGCC 3357
QY 961 CATGAATGCGCATTTCTGACATTTCTGCTCACTGTCAGAAATCTCTCGGAATGAGAGGCA 1020
Db 3356 CATGAATGCGCATTTCTGACATTTCTGCTCACTGTCAGAAATCTCTCGGAATGAGAGGCA 3297
QY 1021 TAGCTTCGTGTGTATGTGTGTTGGGATATTAGCGCTGCTAAACTTTGTGTTCTGATCG 1080
Db 3296 TAGCTTCGTGTGTATGTGTGTTGGGATATTAGCGCTGCTAAACTTTGTGTTCTGATCG 3237
QY 1081 ATCTGTTAGAGAGCATGCTTTTATTAAGCACTTAAAAATGCTAGTATATCTCTCAAGG 1140
Db 3236 ATCTGTTAGAGAGCATGCTTTTATTAAGCACTTAAAAATGCTAGTATATCTCTCAAGG 3177

OY	1141	AGCCTATCTACTGCCAAGGAAGGATACCTTGGCCCTGTGGGATTCAGCCGTTGAAAGGCAAC	1200
Db	3176	AGCCTATCTACTGCCAAGGAAGGATAGCTTGGCCCTGTGGGATTCAGCCGTTGAAAGGCAAC	3117
OY	1201	AAACGATACAGTTACCTTACCAGATGTTTGCCACGACATGGGCAACGTCATGCTAGAC	1260
Db	3116	AAACGATACAGTTACCTTACCAGATGTTTGCCACGACATGGGCAACGTCATGCTAGAC	3057
OY	1261	CAAGAAGGCAAGAACCAAGTTTGTAGCTGTCAAAAAAAGATATGCTAGAGGCTTTCCAGAAT	1320
Db	3056	CAAGAAGGCAAGAACCAAGTTTGTAGCTGTCAAAAAAAGATATGCTAGAGGCTTTCCAGAAT	2997
OY	1321	ATGTTCTATCTCAGCCAGACCAATGGGGGCAAAATTTACTACTAATTTGCCATATCAATTAAC	1380
Db	2996	ATGTTCTATCTCAGCCAGACCAATGGGGGCAAAATTTACTACTAATTTGCCATATCAATTAAC	2937
OY	1381	CACGTAAGAGTCCTTACACTCAACCTTAAGTTGAACGGTCCGTCTCTGGCCACCGTGAG	1440
Db	2936	CACGTAAGAGTCCTTACACTCAACCTTAAGTTGAACGGTCCGTCTCTGGCCACCGTGAG	2877
OY	1441	AATGCAACCTAATGAGCGGGACAAACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGAC	1500
Db	2876	AATGCAACCTAATGAGCGGGACAAACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGAC	2817
OY	1501	GGTGACGCGTGAGGTTGCTTTCGCCATGACCGTCCTTGTTGTTGACGTCACTTCGCGAC	1560
Db	2816	GGTGACGCGTGAGGTTGCTTTCGCCATGACCGTCCTTGTTGTTGACGTCACTTCGCGAC	2757
OY	1561	GCTTGACACCGTGACTTCACCTGCCACACTTGGCCCCCGCGGTGCGCGCGCCTTACAAAGCCA	1620
Db	2756	GCTTGACACCGTGACTTCACCTGCCACACTTGGCCCCCGCGGTGCGCGCGCCTTACAAAGCCA	2697
OY	1621	CACACGCACGCGCGGCCACGATAACCATCTAGCATCCCGGTGTCCACGAAGAGATCCAT	1680
Db	2696	CACACGCACGCGCGGCCACGATAACCATCTAGCATCCCGGTGTCCACGAAGAGATCCAT	2637
OY	1681	CAAGCGTGGCGATG	1695
Db	2636	CAAGCGTGGCGATG	2622

LOCUS	BD013094/c	7492 bp	DNA	linear	PAT 02-AUG-2002
DEFINITION	BD013094 Method for producing male-sterile plant.				
ACCESSION	BD013094				
VERSION	BD013094.1 GI:22093283				
KEYWORDS	WO 0124616-A/5.				
SOURCE	synthetic construct.				
ORGANISM	synthetic construct.				
REFERENCE	artificial sequences.				
AUTHORS	1 (bases 1 to 7492)				
TITLE	Hamada, K. and Nakakido, F.				
JOURNAL	Method for producing male-sterile plant				
COMMENT	patent: WO 0124616-A 5 12-APR-2001;				
	JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO				
	OS Artificial Sequence				
	PN WO 0124616-A/5				
	PD 12-APR-2001				
	PF 12-SEP-2000 WO 2000JP06222				
	PR 30-SEP-1999 JP 99P 279307				
	PI KAZUYUKI HAMADA, FUMIO NAKAKIDO				
	PC A01H5/00, C12N15/11, C12N15/53, C12N15/82				
	CC Plasmid pTS346				
FEATURES	FH Key				
SOURCE	Location/Qualifiers.				
	1. .7492				
BASE COUNT	/organism="synthetic construct"				
ORIGIN	/db_xref="taxon:32630"				
	1987 a 1801 c 1752 g 1952 t				

Query Match	100.0%;	Score 1695;	DB 6;	Length 7492;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1695;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	CCGCAGATCCTCTCTGCTGATGTTTATTAATAATTATATTTACTGGAATACCTACC	60		
Db 5242	CCGCAGATCCTCTCTGCTGATGTTTATTAATAATTATATTTACTGGAATACCTACC	5183		
QY 61	AAATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAATCGCCGACAAATACCAATAGAGA	120		
Db 5182	AAATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAATCGCCGACAAATACCAATAGAGA	5123		
QY 121	TCCAACCACTTAATATCATTAACAACTCTGATTGTTAGTCCAGAACTATATTGAGTAGTG	180		
Db 5122	TCCAACCACTTAATATCATTAACAACTCTGATTGTTAGTCCAGAACTATATTGAGTAGTG	5063		
QY 181	AACAACAATAGCACATTAACATTTAGAGGATTATTGGCTAACCTTGCAATTCAAATATCT	240		
Db 5062	AACAACAATAGCACATTAACATTTAGAGGATTATTGGCTAACCTTGCAATTCAAATATCT	5003		
QY 241	GATGGCTCTAATCTGCTGCAATTTTAAAGCCCTCAGAAAGAAATGCAATCCTTGCAAT	300		
Db 5002	GATGGCTCTAATCTGCTGCAATTTTAAAGCCCTCAGAAAGAAATGCAATCCTTGCAAT	4943		
QY 301	GTTGGCACTGGAAGCTGTCATGTTTATCATCTCTTATTAACGTAGCAAGAGTAGAT	360		
Db 4942	GTTGGCACTGGAAGCTGTCATGTTTATCATCTCTTATTAACGTAGCAAGAGTAGAT	4883		
QY 361	TATATATGTAACAGCAAAATCTCTTCAGATCTCTTCCACATGCAATGTCGTAAGAACAG	420		
Db 4882	TATATATGTAACAGCAAAATCTCTTCAGATCTCTTCCACATGCAATGTCGTAAGAACAG	4823		
QY 421	ATACAGTGTACGTTAGTTTGTAAATGACGGTCAATGCCATTTCTCTGAAGGACATGTTAC	480		
Db 4822	ATACAGTGTACGTTAGTTTGTAAATGACGGTCAATGCCATTTCTCTGAAGGACATGTTAC	4763		
QY 481	AGATGATGATTTCTGGGATCCTTGGAGGGGCCCTGAAATTCGGAACAGTTAGTTAGTT	540		
Db 4762	AGATGATGATTTCTGGGATCCTTGGAGGGGCCCTGAAATTCGGAACAGTTAGTTAGTT	4703		
QY 541	TTAGTACCTAATGTTCTTGGCTTATACATGCTGAATGCCATTTCTCTAAAGCTGAGTTTC	600		
Db 4702	TTAGTACCTAATGTTCTTGGCTTATACATGCTGAATGCCATTTCTCTAAAGCTGAGTTTC	4643		
QY 601	TACCATCTCCACAGCAAAATAAGCTAATACCTGTCCAAAGAGTGGCGGCAATTGACCAA	660		
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Db 4582	ATGAAGATCACAAAGCATGGCCAAAGATGGCAATCTGGCAAAAGAGCGGAATTATATTGAT	4523		
QY 721	TCTACTACATCGAAGCAGAAACCATATACATGTTGGCCCCAGCAAGACCCCCGAGATTAAG	780		
Db 4522	TCTACTACATCGAAGCAGAAACCATATACATGTTGGCCCCAGCAAGACCCCCGAGATTAAG	4463		
QY 781	TTCCGTCTCTCCACAGCAAGATATCCGCAACTGCATAGCTCCCAACAATGAATCCAAA	840		
Db 4462	TTCCGTCTCTCTCCACAGCAAGATATCCGCAACTGCATAGCTCCCAACAATGAATCCAAA	4403		
QY 841	ACCACATCGGGCTCAGAGAGAAGTTATGATTAAGGACACTAATCTGAAATTAATTCTCTAGA	900		
Db 4402	ACCACATCGGGCTCAGAGAGAAGTTATGATTAAGGACACTAATCTGAAATTAATTCTCTAGA	4343		
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Db 4342	AAGCAATTAATATAGCACACCTTGACCTCCACCAAGAGCTTGATGATGACTTGTC	4283		
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Db 4282	CATGAATAGGCATTTGACATTTCTGTCACTGTGACAAATCTCTCGGAAATGAGGAGCA	4223		
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 Db 4222 TAGCTTCCTGCTGTATCTGTGGGATATTACGCTGCTAAACCTTGCTTGTGATCG 4163
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 Db 4162 ATCTGCTTAGAGAGCATGCTCTTTATTAAGCACTTAAATAATGGTAGTATATCTCTCAAGG 4103
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 QY 1681 CAGCGCGTGGCATG 1695
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RESULT 13
 BD010122/c
 ID BD010122 standard; DNA: SYN: 7492 BP.
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 AC BD010122:
 XX
 SV BD010122.1
 XX
 DT 08-FEB-2002 (Rel. 70, Created)
 DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
 XX
 DE Method for producing male-sterile plant.
 XX
 KW JP 03075934-T/5.
 XX
 OS synthetic construct
 OC artificial sequence.
 XX
 RN [1]
 RP 1-7492
 RA Hamada K., Nakakido F.;
 RT "Method for producing male-sterile plant";
 RL Patent number JP03075934-T/5, 16-MAR-2001.
 RL JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO.
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CC OS Artificial Sequence
 CC PN JP 03075934-T/5
 CC PD 16-MAR-2001
 CC PE 12-SEP-2000 JP 2000006222
 CC PR 30-SEP-1999 JP 99P 279307
 CC PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
 CC PC A01H5/00, C12N15/11, C12N15/63, C12N15/82
 CC CC
 CC FH Key Location/Qualifiers
 CC FT source 1. 7492
 CC XX
 FH Key Location/Qualifiers
 FT source 1. 7492
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 FT /organism="synthetic construct"
 SQ Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other:
 Query Match 100.0%; Score 1695; DB 23; Length 7492;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCAGATCCTCTGCTGTGATGTTTATTAATAATTATTAATCTGATACCTACC 60
 Db 5242 CCGCAGATCCTCTGCTGTGATGTTTATTAATAATTATTAATCTGATACCTACC 5183
 QY 61 AATATATAGTACTTGTCAAGCTGCAAGAACTTCCAAATCCGCAATACATAGAGA 120
 Db 5182 AATATATAGTACTTGTCAAGCTGCAAGAACTTCCAAATCCGCAATACATAGAGA 5123
 QY 121 TCCCAACCACTTAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 180
 Db 5122 TCCCAACCACTTAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 5063
 QY 181 AACACAATAGACATTAACATTAATGAGGATTTATGGCTAATCTGCAATTCATATTC 240
 Db 5062 AACACAATAGACATTAACATTAATGAGGATTTATGGCTAATCTGCAATTCATATTC 5003
 QY 241 GATGCGTCTAATCTGCTCAATTTTACGCTCCAGAAAGAAATTCGCAATTCCTGGACAT 300
 Db 5002 GATGCGTCTAATCTGCTCAATTTTACGCTCCAGAAAGAAATTCGCAATTCCTGGACAT 4943
 QY 301 GTTGGCACTGGAATCTGTTGCAATTTTACATCTCTTATTAAGTAGAAGAGTAGAT 360
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 QY 421 ATACAGTGTAGCTTAGTTGTAATGAGCGGTCAATGCCATTTCTGTGAAGGATGTTGAG 480
 Db 4822 ATACAGTGTAGCTTAGTTGTAATGAGCGGTCAATGCCATTTCTGTGAAGGATGTTGAG 4763
 QY 481 AGATGATGATTTCTGGATCCTTGAGGGGCCCTGAATTCGGAACAGTTAGTTGAGTT 540
 Db 4762 AGATGATGATTTCTGGATCCTTGAGGGGCCCTGAATTCGGAACAGTTAGTTGAGTT 4703
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 Db 4702 TTAGTACCTAATGCTTGGCTTATACAGTGAATGCCATTTCTGTAGCTGAGTTTC 4643
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Db	4462	TTCCCTGTTCTTCCACAGCAGAAATATCCGCAACTGCATAGCTCCCAACATGAATCCAAA	4403
QY	841	ACCACATCGGGCTCAGAGAGAAAGTATGATATAAAGGACATTAATCTGATATATTTCTAGA	900
Db	4402	ACCACATCGGGCTCAGAGAGAAAGTATGATATAAAGGACATTAATCTGATATATTTCTAGA	4343
QY	901	AAGCAATTAATATAGCACACACTTGACCTCCACCAAGAAGCTTGTGATCGACTGTGCC	960
Db	4342	AAGCAATTAATATATAGCACACACTTGACCTCCACCAAGAAGCTTGTGATCGACTGTGCC	4283
QY	961	CATGAATATGCAATTTGACATTTCTGCTCAGTGTCAAAATCTCTCGGAAATGAGAGGCA	1020
Db	4282	CATGAATATGCAATTTGACATTTCTGCTCAGTGTCAAAATCTCTCGGAAATGAGAGGCA	4223
QY	1021	TAGCTTCGTGTGTATAGTGTGTGGGATATATACGCTGCTAAACCTTTGTGTTCTGATCG	1080
Db	4222	TAGCTTCGTGTGTATAGTGTGTGGGATATATACGCTGCTAAACCTTTGTGTTCTGATCG	4163
QY	1081	ATCTGTTAGAGAGCATCGCTTTATTAAGCACTTAAATAATGATATATCTCTCAAGG	1140
Db	4162	ATCTGTTAGAGAGCATCGCTTTATTAAGCACTTAAATAATGATATATCTCTCAAGG	4103
QY	1141	AGCCTATACCTGCCAAGAAAGATAGCTTGGCCTGTGGGATTTAGCCGTTGAAGGGAAC	1200
Db	4102	AGCCTATACCTGCCAAGAAAGATAGCTTGGCCTGTGGGATTTAGCCGTTGAAGGGAAC	4043
QY	1201	AAACGAATPACAGTTACCTTACACAGATGTTTSCCAGACATGGGCAACGTCATTGCTAGAC	1260
Db	4042	AAACGAATPACAGTTACCTTACACAGATGTTTSCCAGACATGGGCAACGTCATTGCTAGAC	3983
QY	1261	CAGAAGGCAAGAGCAAAAGTTTACTGTCAAAAAAGATATGCTAGAGCTTTCAGAAAT	1320
Db	3982	CAGAAGGCAAGAGCAAAAGTTTACTGTCAAAAAAGATATGCTAGAGCTTTCAGAAAT	3923
QY	1321	ATGTTCTATCTCAGCCAGAACCAATGGGGCAAAATTTACTACTATTTGCCATVACATTAAC	1380
Db	3922	ATGTTCTATCTCAGCCAGAACCAATGGGGCAAAATTTACTACTATTTGCCATVACATTAAC	3863
QY	1381	CACGTAAGAAGTCTTACACTCAACCTTAACCTGTTGAACGCTCTGTCTTGSCCAACGGTGAG	1440
Db	3862	CACGTAAGAAGTCTTACACTCAACCTTAACCTGTTGAACGCTCTGTCTTGSCCAACGGTGAG	3803
QY	1441	AATGCACCTAATGAGCGGAGAACACACTTCTTTCACCGTGTACTGTCTACATCCTGTAGAC	1500
Db	3802	AATGCACCTAATGAGCGGAGAACACACTTCTTTCACCGTGTACTGTCTACATCCTGTAGAC	3743
QY	1501	GGTGGACGCGTGAGGTGCTTTCGCCATGACCGTCTTGGTGTGTGCAGTCACTTGCGCAC	1560
Db	3742	GGTGGACGCGTGAGGTGCTTTCGCCATGACCGTCTTGGTGTGTGTGCAGTCACTTGCGCAC	3683
QY	1561	GCTTGCACCGGTGACTCACCTGGCACATTTGCCCGCGCGCGTCCGCGGCGCTACAAAAGCCA	1620
Db	3682	GCTTGCACCGGTGACTCACCTGGCACATTTGCCCGCGCGCGTCCGCGGCGCTACAAAAGCCA	3623
QY	1621	CACACGCAACGCGCGCCACAGATTAACCCATCCTAGCATCCCGGTGTCTCAGCAGAGATCCAT	1680
Db	3622	CACACGCAACGCGCGCCACAGATTAACCCATCCTAGCATCCCGGTGTCTCAGCAGAGATCCAT	3563
QY	1681	CAAGCCGTCGCGATG 1695	
Db	3562	CAAGCCGTCGCGATG 3548	
RESULT 14			
A23333	A23333	2407 bp	DNA linear PAT 01-APR-1995
LOCUS	A23333		
DEFINITION	El gene, TATA box and promoter.		
ACCESSION	A23333		

VERSION	A23333.1	GI:904319
KEYWORDS	Oryza sativa.	
SOURCE	Oryza sativa	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.	
FEATURES	<p>location/Qualifiers</p> <p>1..2407</p> <p>/organism="Oryza sativa"</p> <p>/db_xref="taxon:4530"</p> <p><1..>2407</p> <p>1..2263</p> <p>/note="another-specific PE1"</p> <p>2181..2187</p> <p>TATA_signal</p> <p>2264..2407</p> <p>gene</p> <p>/gene="E1"</p> <p>2264..>2407</p> <p>CDS</p> <p>/gene="E1"</p> <p>/codon_start=1</p> <p>/protein_id="CA01673.1"</p> <p>/db_xref="GI:904320"</p> <p>/translation="MTTRPSVFSIVVAIAIALLSLLLIQATPAAASARASKASC</p> <p>DLMO"</p>	
BASE COUNT	662 a	543 c 507 g 695 t
ORIGIN		
Query Match	99.9%	Score 1693.4; DB 6; Length 2407;
Best Local Similarity	99.98%;	Pred. No. 0;
Matches 1694; Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1	CCGCAGATCCTTCTGTGTGATGTTTAAATTTAATATATATATCTGCAATACCTACC 60
DB	572	CCTCAGATCCTTCTGTGTGATGTTTAAATTTAATATATATCTGCAATACCTACC 631
QY	61	AATATATAGTAGACTTGTCAAGCTGCAGAACTTCCAAATGCGCCAAATACCAATAGAGA 120
DB	632	AATATATAGTAGACTTGTCAAGCTGCAGAACTTCCAAATGCGCCAAATACCAATAGAGA 691
QY	121	TCCAACCACTTAATATATCATTAACAATCTGATTTGTTAGTCCAGAACTATATTGAGTAGTG 180
DB	692	TCCAACCACTTAATATATCATTAACAATCTGATTTGTTAGTCCAGAACTATATTGAGTAGTG 751
QY	181	AACAACAATAGCACTTAACATTTATGAGATTTATGAGCTAAGCTGCAATTCATATTTCT 240
DB	752	AACAACAATAGCACTTAACATTTATGAGATTTATGAGCTAAGCTGCAATTCATATTTCT 911
QY	241	GATGCGTCTAATCTGTCAATTTTAGCGCTCCAGAAAGAAATTTGCAATCTTGGACAAT 300
DB	812	GATGCGTCTAATCTGTCAATTTTAGCGCTCCAGAAAGAAATTTGCAATCTTGGACAAT 871
QY	301	GTTGGCACTGGAACTGTTGCATGTTTTCATCTCTTATTTACGTAAGCAAGAGTAGAT 360
DB	872	GTTGGCACTGGAACTGTTGCATGTTTTCATCTCTTATTTACGTAAGCAAGAGTAGAT 931
QY	361	TATTATGTACAGAGAAATCTCTTCAGATCTTTCACATGCAATGTCGTAAGAAGACAG 420
DB	932	TATTATGTACAGAGAAATCTCTTCAGATCTTTCACATGCAATGTCGTAAGAAGACAG 991
QY	421	ATACAGTGTACGTTAGTTTGTAAATGAGAGCGTCAATGCGCATTTCTCTGAAGGATGTCAG 480
DB	992	ATACAGTGTACGTTAGTTTGTAAATGAGAGCGTCAATGCGCATTTCTCTGAAGGATGTCAG 1051
QY	481	AGATGATGATTTCTGGGATCTTGGAGGGGCGCGTGAATTCGGAATTCAGTTGAGTT 540
DB	1052	AGATGATGATTTCTGGGATCTTGGAGGGGCGCGTGAATTCGGAATTCAGTTGAGTT 1111
QY	541	TTAGTACCTAATGTTCTTGGCTTATCTAGCTGAATGCAATTTCTGTAAGCTGAGTTTC 600
DB	1112	TTAGTACCTAATGTTCTTGGCTTATCTAGCTGAATGCAATTTCTGTAAGCTGAGTTTC 1171
QY	601	TACCATCTCCACAGAAATAAGCTAATACCTGTCCAGAGAGTGTGCGGCATTTGACCA 660

Db	1172	TACCATCTCCACAGGAATTAAGCTAATACCTGTCCAAAGATGGTCCGGCAATTTGACCAA	1231
QY	661	ATGAAGATCAGAACGATGGCAAGAAATGGCAATCTGGCAAAAGACCGGAATTAATTTGTAAT	720
Db	1232	ATGAAGATCAGAACGATGGCAAGAAATGGCAATCTGGCAAAAGACCGGAATTAATTTGTAAT	1291
QY	721	TCCTACTACATGCAACAGAACCATATGTAATGTTGCCCCAGCAAGAACCCCGGACAGATAAG	780
Db	1292	TCCTACTACATGCAACAGAACCATATGTAATGTTGCCCCAGCAAGAACCCCGGACAGATAAG	1351
QY	781	TTCCCTGTTCTTCCACAGCAAGATATCCGCCAATCTGATAGCTCCCAACAATGAAATCCAAA	840
Db	1352	TTCCCTGTTCTTCCACAGCAAGATATCCGCCAATCTGATAGCTCCCAACAATGAAATCCAAA	1411
QY	841	ACCAATCTGGCTCAGACAGAAAGTTATGATTAATAAGGCACTAATCTGATTAATTTCTTAGA	900
Db	1412	ACCAATCTGGCTCAGACAGAAAGTTATGATTAATAAGGCACTAATCTGATTAATTTCTTAGA	1471
QY	901	AAGCGAATTAATAGACACACCTTGACCTCCACCAAGAGCTTTGTGATCCACTTGTGCC	960
Db	1472	AAGCGAATTAATAGACACACCTTGACCTCCACCAAGAGCTTTGTGATCCACTTGTGCC	1531
QY	961	CATGAATGGCAATCTGACATCTGTGATCAGATCTCTCGGAAATGAGAGGCA	1020
Db	1532	CATGAATGGCAATCTGACATCTGTGATCAGATCTCTCGGAAATGAGAGGCA	1591
QY	1021	TAGCTTCGTGTGTATGTGTGGGATTAATACCTGTCTAAACTTTGTGTTTCTGATCG	1080
Db	1592	TAGCTTCGTGTGTATGTGTGGGATTAATACCTGTCTAAACTTTGTGTTTCTGATCG	1651
QY	1081	ATCTGTTAGAGAGCATCTCTTATTAAGCACTTAAAAATGATTAATCTCTCAAGG	1140
Db	1652	ATCTGTTAGAGAGCATCTCTTATTAAGCACTTAAAAATGATTAATCTCTCAAGG	1711
QY	1141	AGCCTATACCTGCCAAGAAAGATACCTTGGCCTGTGGGANTGAGCCGTGAAGGGAAC	1200
Db	1712	AGCCTATACCTGCCAAGAAAGATACCTTGGCCTGTGGGANTGAGCCGTGAAGGGAAC	1771
QY	1201	AAAGCAATACAGTTACCTTACCGAGATGTTTCCACGACATGGGCAACGTCATTTGCTAGAC	1260
Db	1772	AAAGCAATACAGTTACCTTACCGAGATGTTTCCACGACATGGGCAACGTCATTTGCTAGAC	1831
QY	1261	CAAGAGGCAAGAGCAAAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTCCAGAAAT	1320
Db	1832	CAAGAGGCAAGAGCAAAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTCCAGAAAT	1891
QY	1321	ATGTTCTATCTCAGCCAGAACCAATGGGGGCAAAATTTACTACTATTTGCCATACATTAAC	1380
Db	1892	ATGTTCTATCTCAGCCAGAACCAATGGGGGCAAAATTTACTACTATTTGCCATACATTAAC	1951
QY	1381	CACGTAAAAGTCTCTACACTCAACCTTAACCTGTTGAACGGTCTGTTCTGGCCAAAGGTGAG	1440
Db	1952	CACGTAAAAGTCTCTACACTCAACCTTAACCTGTTGAACGGTCTGTTCTGGCCAAAGGTGAG	2011
QY	1441	AATGCACCTAATGAGAGGAGACAACACTTCTTCAACCGTGTACTGTACTACTCTGTAGAC	1500
Db	2012	AATGCACCTAATGAGAGGAGACAACACTTCTTCAACCGTGTACTGTACTACTCTGTAGAC	2071
QY	1501	GGTGGACGGGTGAGGTCTTTCGCCATGACCGTCTTGGTTGTTGACAGTCACTTGGCCAC	1560
Db	2072	GGTGGACGGGTGAGGTCTTTCGCCATGACCGTCTTGGTTGTTGACAGTCACTTGGCCAC	2131
QY	1561	GCTTGACCGCTGACTCACTTGCACATTTGCCCGCCCGCTGCCCGGCGCTTACAAGGCCA	1620
Db	2132	GCTTGACCGCTGACTCACTTGCACATTTGCCCGCCCGCTGCCCGGCGCTTACAAGGCCA	2191
QY	1621	CACAGGCAAGCGCGGCCACGATAACGCAATCTGATGATCCCGGTGTCACAGAGAGATCCAT	1680
Db	2192	CACAGGCAAGCGCGGCCACGATAACGCAATCTGATGATCCCGGTGTCACAGAGAGATCCAT	2251
QY	1681	CAAGCCGTCGGCATG 1695	
Db	2252	CAAGCCGTCGGCATG 2266	

RESULT 15	AR007519	2407 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR007519	Sequence 9 from patent US 5750867.			
DEFINITION	AR007519				
ACCESSION	AR007519.1	GI:3967003			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2407)				
AUTHORS	Williams, M. and Leeemans, J.				
TITLE	Maintenance of male-sterile plants				
JOURNAL	Patent: US 5750867-A 9 12-May-1998;				
FEATURES	location/Qualifiers				
source	1..2407				
BASE COUNT	662 a 543 c 507 g 695 t				
ORIGIN	/organism="unknown"				
Query Match	99.98%; Score 1693.4; DB 6; Length 2407;				
Best Local Similarity	99.98%; Pred. No. 0;				
Matches 1694; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
QY	1	CCGCGATCCCTTCTGTGTGATGTTTATTAATAATTTATATTTATCTGCAATACCTACC	60		
Db	572	CCGCGATCCCTTCTGTGTGATGTTTATTAATAATTTATATTTATCTGGAATACCTACC	631		
QY	61	AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAAATCGCCGCAATACCAATAGAGA	120		
Db	632	AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAAATCGCCGCAATACCAATAGAGA	691		
QY	121	TCCAAACCACTTAATATATCAATAACATCTGATTTGTTAGTCCAGAACTATATTGAGTAGTG	180		
Db	692	TCCAAACCACTTAATATATCAATAACATCTGATTTGTTAGTCCAGAACTATATTGAGTAGTG	751		
QY	181	AACAACAATAGCAATTAACATTAATGAGATTAATGGCTAACCTCTGCAATTCATATATCT	240		
Db	752	AACAACAATAGCAATTAACATTAATGAGATTAATGGCTAACCTCTGCAATTCATATATCT	811		
QY	241	GATGCGCTAATCTGTGCAATTTTACGGCTCCAGAAAGAAATGCAACAATCCTTGCAAAAT	300		
Db	812	GATGCGCTAATCTGTGCAATTTTACGGCTCCAGAAAGAAATGCAACAATCCTTGCAAAAT	871		
QY	301	GTGGCAGCTGGAAGCTGTGCATGTTTTCACATCTCTTATTAACGTAGCAAGAGGTAGAT	360		
Db	872	GTGGCAGCTGGAAGCTGTGCATGTTTTCACATCTCTTATTAACGTAGCAAGAGGTAGAT	931		
QY	361	TATTATGTACAGGAGAAATCTCTTCAGATCTTCCACATGCAATGTCTGAAGAAGACAG	420		
Db	932	TATTATGTACAGGAGAGAAATCTCTTCAGATCTTCCACATGCAATGTCTGAAGAAGACAG	991		
QY	421	ATACAGTGTACCTTAGTTGTATGAGAGGGTCAATGCCATTTCTCTGAAGGCATGTTGAG	480		
Db	992	ATACAGTGTACCTTAGTTGTATGAGAGGGTCAATGCCATTTCTCTGAAGGCATGTTGAG	1051		
QY	481	AGATGATGATTTCTGGGATCTTGGAGGGGCCCTCAAAATTCGAAACAGTTAGTTGAGTT	540		
Db	1052	AGATGATGATTTCTGGGATCTTGGAGGGGCCCTCAAAATTCGAAACAGTTAGTTGAGTT	1111		
QY	541	TTAGTACCTAATGTCTTGGCTTATACTACGTGAATGCCATTTCTGTAAAGCTGAGTTTTC	600		
Db	1112	TTAGTACCTAATGTCTTGGCTTATACTACGTGAATGCCATTTCTGTAAAGCTGAGTTTTC	1171		
QY	601	TACCATCTCCACAGGAATAAGCTAATAACCTGTCACAGAGTGGTGGCGCATTTGACCAA	660		
Db	1172	TACCATCTCCACAGGAATAAGCTAATAACCTGTCACAGAGTGGTGGCGCATTTGACCAA	1231		
QY	661	ATGAAGATCAGAACGATGGCAAGAAATGCGCAATCTGGCAAGAGAGCGGAATTAATTTGAT	720		
Db	1232	ATGAAGATCAGAACGATGGCAAGAAATGCGCAATCTGGCAAGAGAGCGGAATTAATTTGAT	1291		

QY 721 TCTACTACATCGAACAGGAACCATATCAATGTGGCCAGCAAGGACCCCGCAGATAAG 780
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Db 1292 TCTACTACATCGAACAGGAACCATATCAATGTGGCCAGCAAGGACCCCGCAGATAAG 1351
QY 781 TTCCTGTCTTCCACAGCAGAGATATCCGCACTGCATAGCTCCCAACATGAATCCAAA 840
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Db 1352 TTCCTGTCTTCCACAGCAGAGATATCCGCACTGCATAGCTCCCAACATGAATCCAAA 1411
QY 841 ACCACATCGGCTCAGAGAGAGTATGATAAAAGGCACCTAATTCTGAATTAATTCCTAGA 900
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Db 1412 ACCACATCGGCTCAGAGAGAGTATGATAAAAGGCACCTAATTCTGAATTAATTCCTAGA 1471
QY 901 AAGCGAATAATATAGCACACCTTGACCTCCACCAAGAGCTTGTGATCGACTGTGCC 960
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Db 1472 AAGCGAATAATATAGCACACCTTGACCTCCACCAAGAGCTTGTGATCGACTGTGCC 1531
QY 961 CATGAAATGGCATTTCTGACATTTCTGTCACCTGTCAAGATCTCTCGAAATAGAGAGCA 1020
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Db 1532 CATGAAATGGCATTTCTGACATTTCTGTCACCTGTCAAGATCTCTCGAAATAGAGAGCA 1591
QY 1021 TAGCTTCGTGTGTATGTGTGTGGATATTACGCTGCTAAAACCTTGTGTCTGATCG 1080
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Db 1592 TAGCTTCGTGTGTATGTGTGTGGATATTACGCTGCTAAAACCTTGTGTCTGATCG 1651
QY 1081 ATCTGGTTAGAGACATCGTCTTTATAGCACTTAAAATGCTAGTATATCTCTCAAG 1140
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Db 1652 ATCTGGTTAGAGACATCGTCTTTATAGCACTTAAAATGCTAGTATATCTCTCAAG 1711
QY 1141 AGCCTATCTGCCAAGGAAAGGATAGCTTGGCCTGTGGGATTGAGCCGTTGAAGGGAAC 1200
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Db 1712 AGCCTATCTGCCAAGGAAAGGATAGCTTGGCCTGTGGGATTGAGCCGTTGAAGGGAAC 1771
QY 1201 AAACGAATACAGTTACCTTACCAGATGTTGGCAGACATGGGCAACGTCATTGCTAGAC 1260
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Db 1772 AAACGAATACAGTTACCTTACCAGATGTTGGCAGACATGGGCAACGTCATTGCTAGAC 1831
QY 1261 CAAGAAGGCAAGAAGCAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTTCCAGAAT 1320
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Db 1832 CAAGAAGGCAAGAAGCAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTTCCAGAAT 1891
QY 1321 ATGTTCTATCTCAGCCAGACCAATGGGGCAAAATTACTACTATTTGCCATATCAATTAAC 1380
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Db 1892 ATGTTCTATCTCAGCCAGACCAATGGGGCAAAATTACTACTATTTGCCATATCAATTAAC 1951
QY 1381 CACGTAAAGTCCCTACACTCAACCTACTGTGAACGGTCTCTGTGGCCAACGGTGAG 1440
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Db 1952 CACGTAAAGTCCCTACACTCAACCTACTGTGAACGGTCTCTGTGGCCAACGGTGAG 2011
QY 1441 AATGCACCTAATGGACGGGACAACACTCTCTTTCACCGCTGCTACTGCTACATCTGTAGAC 1500
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Db 2012 AATGCACCTAATGGACGGGACAACACTCTCTTTCACCGCTGCTACTGCTACATCTGTAGAC 2071
QY 1501 GGTGGACGGGTGAGGTCTTTCGCCATGACCCGCTTGTGTTGTCAGTCACTTGGCCAC 1560
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Db 2072 GGTGGACGGGTGAGGTCTTTCGCCATGACCCGCTTGTGTTGTCAGTCACTTGGCCAC 2131
QY 1561 GCTTGACCCGTGACTGACCTGACCACATTTGCCCGCCGCTGCGGCGCTACAAAAGCCA 1620
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Db 2132 GCTTGACCCGTGACTGACCTGACCACATTTGCCCGCCGCTGCGGCGCTACAAAAGCCA 2191
QY 1621 CACACGACAGCGCGCACGATTAACCCATCTAGCATCCGGGTGTCCAGCAAGAGATCCAT 1680
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Db 2192 CACACGACAGCGCGCACGATTAACCCATCTAGCATCCGGGTGTCCAGCAAGAGATCCAT 2251
QY 1681 CAAGCCGTGCGGATG 1695
|||||
Db 2252 CAAGCCGTGCGGATG 2266

